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1600

RAW SEQUENCE LISTING

DATE: 05/06/2003

PATENT APPLICATION: US/09/652,292C

TIME: 12:01:33

Input Set : A:\EP.txt

Output Set: N:\CRF4\05062003\I652292C.raw

3 <110> APPLICANT: Bowden, Donald W.
4 Dawson, Paul A.
5 Fossey, Sallyanne C.
7 <120> TITLE OF INVENTION: GLUT10: A Novel Glucose Transporter in the Type 2 Diabetes
Linked
8 Region of Chromosome 20Q12-13.1
10 <130> FILE REFERENCE: 9151-11
12 <140> CURRENT APPLICATION NUMBER: US 09/652,292C
13 <141> CURRENT FILING DATE: 2000-08-31
15 <160> NUMBER OF SEQ ID NOS: 43
17 <170> SOFTWARE: PatentIn version 3.2
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 4395
21 <212> TYPE: DNA
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34 cagggcagga gggacagagg cggggcggg cgggaaagt ttgtccggcg cagcggcggtt 180
36 ggggactccg gcgggggatg cgcgcccggc ccctcagcgc ccccgacag cgcgcgagtc 240
38 ccgctcgcc atg ggc cac tcc cca cct gtc ctg cct ttg tgt gcc tct gtg 291
39 Met Gly His Ser Pro Val Leu Pro Leu Cys Ala Ser Val
40 1 5 10
42 tct ttg ctg ggt ggc ctg acc ttt ggt tat gaa ctg gca gtc ata tca 339
43 Ser Leu Leu Gly Gly Leu Thr Phe Gly Tyr Glu Leu Ala Val Ile Ser
44 15 20 25 30
46 ggt gcc ctg ctg cca ctg cag ctt gac ttt ggg cta agc tgc ttg gag 387
47 Gly Ala Leu Leu Pro Leu Gln Leu Asp Phe Gly Leu Ser Cys Leu Glu
48 35 40 45
50 cag gag ttc ctg gtg ggc agc ctg ctg ctg ggg gct ctc ctc gcc tcc 435
51 Gln Glu Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser
52 50 55 60
54 ctg gtt ggt ggc ttc ctc att gac tgc tat ggc agg aag caa gcc atc 483
55 Leu Val Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile
56 65 70 75
58 ctc ggg agc aac ttg gtg ctg ctg gca ggc agc ctg acc ctg ggc ctg 531
59 Leu Gly Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu
60 80 85 90
62 gct ggt tcc ctg gcc tgg ctg gtc ctg ggc cgc gct gtg gtt ggc ttc 579
63 Ala Gly Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe
64 95 100 105 110

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66 gcc att tcc ctc tcc tcc atg gct tgc tgt atc tac gtg tca gag ctg      627
67 Ala Ile Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu
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70 gtg ggg cca cgg cag cgg gga gtg ctg gtg tcc ctc tat gag gca ggc      675
71 Val Gly Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly
72              130              135              140
74 atc acc gtg ggc atc ctg ctc tcc tat gcc ctc aac tat gca ctg gct      723
75 Ile Thr Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala
76              145              150              155
78 ggt acc ccc tgg gga tgg agg cac atg ttc ggc tgg gcc act gca cct      771
79 Gly Thr Pro Trp Gly Trp Arg His Met Phe Gly Trp Ala Thr Ala Pro
80              160              165              170
82 gct gtc ctg caa tcc ctc agc ctc ctc ttc ctc cct gct ggt aca gat      819
83 Ala Val Leu Gln Ser Leu Ser Leu Leu Phe Leu Pro Ala Gly Thr Asp
84 175              180              185              190
86 gag act gca aca cac aag gac ctc atc cca ctc cag gga ggt gag gcc      867
87 Glu Thr Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala
88              195              200              205
90 ccc aag ctg ggc ccg ggg agg cca cgg tac tcc ttt ctg gac ctc ttc      915
91 Pro Lys Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe
92              210              215              220
94 agg gca cgc gat aac atg cga ggc cgg acc aca gtg ggc ctg ggg ctg      963
95 Arg Ala Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu
96              225              230              235
98 gtg ctc ttc cag caa cta aca ggg cag ccc aac gtg ctg tgc tat gcc      1011
99 Val Leu Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala
100              240              245              250
102 tcc acc atc ttc agc tcc gtt ggt ttc cat ggg gga tcc tca gcc gtg      1059
103 Ser Thr Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val
104 255              260              265              270
106 ctg gcc tct gtg ggg ctt ggc gca gtg aag gtg gca gct acc ctg acc      1107
107 Leu Ala Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr
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110 gcc atg ggg ctg gtg gac cgt gca ggc cgc agg gct ctg ttg cta gct      1155
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114 ggc tgt gcc ctc atg gcc ctg tcc gtc agt ggc ata ggc ctc gtc agc      1203
115 Gly Cys Ala Leu Met Ala Leu Ser Val Ser Gly Ile Gly Leu Val Ser
116              305              310              315
118 ttt gcc gtg ccc atg gac tca ggc cca agc tgt ctg gct gtg ccc aat      1251
119 Phe Ala Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn
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122 gcc acc ggg cag aca ggc ctc cct gga gac tct ggc ctg ctg cag gac      1299
123 Ala Thr Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp
124 335              340              345              350
126 tcc tct cta cct ccc att cca agg acc aat gag gac caa agg gag cca      1347
127 Ser Ser Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro
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130 atc ttg tcc act gct aag aaa acc aag ccc cat ccc aga tct gga gac      1395

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134	ccc	tca	gcc	cct	cct	cgg	ctg	gcc	ctg	agc	tct	gcc	ctc	cct	ggg	ccc	1443
135	Pro	Ser	Ala	Pro	Pro	Arg	Leu	Ala	Leu	Ser	Ser	Ala	Leu	Pro	Gly	Pro	
136			385					390					395				
138	cct	ctg	ccc	gct	cgg	ggg	cat	gca	ctg	ctg	cgc	tgg	acc	gca	ctg	ctg	1491
139	Pro	Leu	Pro	Ala	Arg	Gly	His	Ala	Leu	Leu	Arg	Trp	Thr	Ala	Leu	Leu	
140		400					405					410					
142	tgc	ctg	atg	gtc	ttt	gtc	agt	gcc	ttc	tcc	ttt	ggg	ttt	ggg	cca	gtg	1539
143	Cys	Leu	Met	Val	Phe	Val	Ser	Ala	Phe	Ser	Phe	Gly	Phe	Gly	Pro	Val	
144	415					420					425					430	
146	acc	tgg	ctt	gtc	ctc	agc	gag	atc	tac	cct	gtg	gag	ata	cga	gga	aga	1587
147	Thr	Trp	Leu	Val	Leu	Ser	Glu	Ile	Tyr	Pro	Val	Glu	Ile	Arg	Gly	Arg	
148					435					440					445		
150	gcc	ttc	gcc	ttc	tgc	aac	agc	ttc	aac	tgg	gcg	gcc	aac	ctc	ttc	atc	1635
151	Ala	Phe	Ala	Phe	Cys	Asn	Ser	Phe	Asn	Trp	Ala	Ala	Asn	Leu	Phe	Ile	
152				450					455					460			
154	agc	ctc	tcc	ttc	ctc	gat	ctc	att	ggc	acc	atc	ggc	ttg	tcc	tgg	acc	1683
155	Ser	Leu	Ser	Phe	Leu	Asp	Leu	Ile	Gly	Thr	Ile	Gly	Leu	Ser	Trp	Thr	
156			465					470					475				
158	ttc	ctg	ctc	tac	gga	ctg	acc	gct	gtc	ctc	ggc	ctg	ggc	ttc	atc	tat	1731
159	Phe	Leu	Leu	Tyr	Gly	Leu	Thr	Ala	Val	Leu	Gly	Leu	Gly	Phe	Ile	Tyr	
160		480					485					490					
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163	Leu	Phe	Val	Pro	Glu	Thr	Lys	Gly	Gln	Ser	Leu	Ala	Glu	Ile	Asp	Gln	
164	495					500				505					510		
166	cag	ttc	cag	aag	aga	cgg	ttc	acc	ctg	agc	ttt	ggc	cac	agg	cag	aac	1827
167	Gln	Phe	Gln	Lys	Arg	Phe	Thr	Leu	Ser	Phe	Gly	His	Arg	Gln	Asn		
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216 tcagatgggg gactgagcaa gtagctatga ctgcagatca tgtaagggaag ggactgacaa 3195
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262 <213> ORGANISM: Homo sapiens

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271 20 25 30
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275 35 40 45
278 Phe Leu Val Gly Ser Leu Leu Leu Gly Ala Leu Leu Ala Ser Leu Val
279 50 55 60
282 Gly Gly Phe Leu Ile Asp Cys Tyr Gly Arg Lys Gln Ala Ile Leu Gly
283 65 70 75 80
286 Ser Asn Leu Val Leu Leu Ala Gly Ser Leu Thr Leu Gly Leu Ala Gly
287 85 90 95
290 Ser Leu Ala Trp Leu Val Leu Gly Arg Ala Val Val Gly Phe Ala Ile
291 100 105 110
294 Ser Leu Ser Ser Met Ala Cys Cys Ile Tyr Val Ser Glu Leu Val Gly
295 115 120 125
298 Pro Arg Gln Arg Gly Val Leu Val Ser Leu Tyr Glu Ala Gly Ile Thr
299 130 135 140
302 Val Gly Ile Leu Leu Ser Tyr Ala Leu Asn Tyr Ala Leu Ala Gly Thr

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311          180          185          190
314 Ala Thr His Lys Asp Leu Ile Pro Leu Gln Gly Gly Glu Ala Pro Lys
315          195          200          205
318 Leu Gly Pro Gly Arg Pro Arg Tyr Ser Phe Leu Asp Leu Phe Arg Ala
319          210          215          220
322 Arg Asp Asn Met Arg Gly Arg Thr Thr Val Gly Leu Gly Leu Val Leu
323 225          230          235          240
326 Phe Gln Gln Leu Thr Gly Gln Pro Asn Val Leu Cys Tyr Ala Ser Thr
327          245          250          255
330 Ile Phe Ser Ser Val Gly Phe His Gly Gly Ser Ser Ala Val Leu Ala
331          260          265          270
334 Ser Val Gly Leu Gly Ala Val Lys Val Ala Ala Thr Leu Thr Ala Met
335          275          280          285
338 Gly Leu Val Asp Arg Ala Gly Arg Arg Ala Leu Leu Leu Ala Gly Cys
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343 305          310          315          320
346 Val Pro Met Asp Ser Gly Pro Ser Cys Leu Ala Val Pro Asn Ala Thr
347          325          330          335
350 Gly Gln Thr Gly Leu Pro Gly Asp Ser Gly Leu Leu Gln Asp Ser Ser
351          340          345          350
354 Leu Pro Pro Ile Pro Arg Thr Asn Glu Asp Gln Arg Glu Pro Ile Leu
355          355          360          365
358 Ser Thr Ala Lys Lys Thr Lys Pro His Pro Arg Ser Gly Asp Pro Ser
359          370          375          380
362 Ala Pro Pro Arg Leu Ala Leu Ser Ser Ala Leu Pro Gly Pro Pro Leu
363 385          390          395          400
366 Pro Ala Arg Gly His Ala Leu Leu Arg Trp Thr Ala Leu Leu Cys Leu
367          405          410          415
370 Met Val Phe Val Ser Ala Phe Ser Phe Gly Phe Gly Pro Val Thr Trp
371          420          425          430
374 Leu Val Leu Ser Glu Ile Tyr Pro Val Glu Ile Arg Gly Arg Ala Phe
375          435          440          445
378 Ala Phe Cys Asn Ser Phe Asn Trp Ala Ala Asn Leu Phe Ile Ser Leu
379          450          455          460
382 Ser Phe Leu Asp Leu Ile Gly Thr Ile Gly Leu Ser Trp Thr Phe Leu
383 465          470          475          480
386 Leu Tyr Gly Leu Thr Ala Val Leu Gly Leu Gly Phe Ile Tyr Leu Phe
387          485          490          495
390 Val Pro Glu Thr Lys Gly Gln Ser Leu Ala Glu Ile Asp Gln Gln Phe
391          500          505          510
394 Gln Lys Arg Arg Phe Thr Leu Ser Phe Gly His Arg Gln Asn Ser Thr
395          515          520          525
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